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RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/719,692
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RAW SEQUENCE LISTING DATE: 03/18/2005
PATENT APPLICATION: **US/10/719,692** TIME: 08:55:32

Input Set : **N:\Crf4\Refhold\10_folder\J719692.raw**
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<110> APPLICANT: An, Songzhu
Chen, Jin-Long
Tian, Hui
Zhong, Wendy Wen
Tularik Inc.
<120> TITLE OF INVENTION: Receptor Ligands and Methods of Modulating Receptors
<130> FILE REFERENCE: 018781-009530US
<140> CURRENT APPLICATION NUMBER: US/10/719,692
<141> CURRENT FILING DATE: 2003-11-21
<150> PRIOR APPLICATION NUMBER: US 60/421,142
<151> PRIOR FILING DATE: 2002-11-25
<150> PRIOR APPLICATION NUMBER: US 60/444,153
<151> PRIOR FILING DATE: 2003-01-30
<160> NUMBER OF SEQ ID NOS: 9
<170> SOFTWARE: PatentIn Ver. 2.1
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<211> LENGTH: 1164
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: human G-protein coupled receptor TGR4a (HM74)
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gggcttctgg gcaatggcct tgccctgtgg attttctgtt tccacctcaa gtcctggaaa 180
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gtggcggtag acaggtattt ccgggtggtc catccccacc acgccctgaa caagatctcc 420
aattggacag cagccatcat ctcttgcctt ctgtggggca tcactgttgg cctaacagtc 480
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<211> LENGTH: 387
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            20                  25                  30
Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
        35                  40                  45
Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
    50                  55                  60
Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
65                  70                  75                  80
Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Asn Phe Gly
                85                  90                  95
Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln
            100                 105                 110
Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg
        115                 120                 125
Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala
    130                 135                 140
Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val
145                 150                 155                 160
His Leu Leu Lys Lys Lys Leu Leu Ile Gln Asn Gly Pro Ala Asn Val
                165                 170                 175
Cys Ile Ser Phe Ser Ile Cys His Thr Phe Arg Trp His Glu Ala Met
            180                 185                 190
Phe Leu Leu Glu Phe Leu Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser
        195                 200                 205
Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala
    210                 215                 220
Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe
225                 230                 235                 240
Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp
                245                 250                 255
Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val
            260                 265                 270
Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
        275                 280                 285
Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe
    290                 295                 300
Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu
305                 310                 315                 320
Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn
                325                 330                 335
Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro
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Input Set : N:\Crf4\Refhold\10_folder\J719692.raw
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96       Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Asn Asn His Ser Lys Lys
97               355                 360                 365
98       Gly His Cys His Gln Glu Pro Ala Ser Leu Glu Lys Gln Leu Gly Cys
99           370                 375                 380
100       Cys Ile Glu
101       385
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104 <211> LENGTH: 1092
105 <212> TYPE: DNA
106 <213> ORGANISM: Homo sapiens
107 <220> FEATURE:
108 <223> OTHER INFORMATION: human G-protein coupled receptor TGR4b
109 <400> SEQUENCE: 3
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111       ttccgagatg acttcattgt caaggtgttg ccgccggtgt tggggctgga gtttatcttc 120
112       gggcttctgg gcaatggcct tgccctgtgg attttctgtt tccacctcaa gtcctggaaa 180
113       tccagccgga ttttcctgtt caacctggca gtggctgact ttctactgat catctgcctg 240
114       cccttcctga tggacaacta tgtgaggcgt tgggactgga agtttgggga catcccttgc 300
115       cggctgatgc tcttcatgtt ggctatgaac cgccagggca gcatcatctt cctcacggtg 360
116       gtggcggtag acaggtattt ccgggtggtc catccccacc acgccctgaa caagatctcc 420
117       aatcggacag cagccatcat ctcttgcctt ctgtggggca tcactattgg cctgacagtc 480
118       cacctcctga agaagaagat gccgatccag aatggcggtg caaatttgtg cagcagcttc 540
119       agcatctgcc ataccttcca gtggcacgaa gccatgttcc tcctggagtt cttcctgccc 600
120       ctgggcatca tcctgttctg ctcagccaga attatctgga gcctgcggca gagacaaatg 660
121       gaccggcatg ccaagatcaa gagagccatc accttcatca tggtggtggc catcgtcttt 720
122       gtcatctgct tccttcccag cgtggttgtg cggatccgca tcttctggct cctgcacact 780
123       tcgggcacgc agaattgtga agtgtaccgc tcggtggacc tggcgttctt tatcactctc 840
124       agcttcacct acatgaacag catgctggac cccgtggtgt actacttctc cagcccatcc 900
125       tttcccaact tcttctccac tttgatcaac cgctgcctcc agaggaagat gacaggtgag 960
126       ccagataata accgcagcac gagcgtcgag ctcacagggg accccaacaa aaccagaggc 1020
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128       acctctcctt aa                                                    1092
130 <210> SEQ ID NO: 4
131 <211> LENGTH: 363
132 <212> TYPE: PRT
133 <213> ORGANISM: Homo sapiens
134 <220> FEATURE:
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140                    20                  25                  30
141       Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
142                35                  40                  45
143       Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
144            50                  55                  60
145       Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
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Input Set : N:\Crf4\Refhold\10_folder\J719692.raw
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146        65                  70                  75                  80
147       Pro Phe Leu Met Asp Asn Tyr Val Arg Arg Trp Asp Trp Lys Phe Gly
148                        85                  90                  95
149       Asp Ile Pro Cys Arg Leu Met Leu Phe Met Leu Ala Met Asn Arg Gln
150                   100                 105                 110
151       Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg
152               115                 120                 125
153       Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Arg Thr Ala
154           130                 135                 140
155       Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Ile Gly Leu Thr Val
156       145                 150                 155                 160
157       His Leu Leu Lys Lys Lys Met Pro Ile Gln Asn Gly Gly Ala Asn Leu
158                       165                 170                 175
159       Cys Ser Ser Phe Ser Ile Cys His Thr Phe Gln Trp His Glu Ala Met
160                   180                 185                 190
161       Phe Leu Leu Glu Phe Phe Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser
162               195                 200                 205
163       Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala
164           210                 215                 220
165       Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe
166       225                 230                 235                 240
167       Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp
168                       245                 250                 255
169       Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val
170                   260                 265                 270
171       Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
172               275                 280                 285
173       Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe
174           290                 295                 300
175       Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu
176       305                 310                 315                 320
177       Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn
178                       325                 330                 335
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185 <211> LENGTH: 1041
186 <212> TYPE: DNA
187 <213> ORGANISM: Homo sapiens
188 <220> FEATURE:
189 <223> OTHER INFORMATION: human G-protein coupled receptor TGR183
190 <400> SEQUENCE: 5
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193       tgcttccaca tgaagacctg gaagcccagc actgtttacc ttttcaattt ggccgtggct 180
194       gatttcctcc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac 240
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caccacgcgg tgaacactat ctccacccgg gtggcggctg gcatcgtctg caccctgtgg 420
gccctggtca tcctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag 480
acggccgtct cctgtgagag cttcatcatg gagtcggcca atggctggca tgacatcatg 540
ttccagctgg agttctttat gcccctcggc atcatcttat tttgctcctt caagattgtt 600
tggagcctga ggcggaggca gcagctggcc agacaggctc ggatgaagaa ggcgacccgg 660
ttcatcatgg tggtggcaat tgtgttcatc acatgctacc tgcccagcgt gtctgctaga 720
ctctatttcc tctggacggt gccctcgagt gcctgcgatc cctctgtcca tggggccctg 780
cacataaccc tcagcttcac ctacatgaac agcatgctgg atcccctggt gtattatttt 840
tcaagccccc cctttcccaa attctacaac aagctcaaaa tctgcagtct gaaacccaag 900
cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcgaa cctcggtcgc 960
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<213> ORGANISM: Homo sapiens
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<400> SEQUENCE: 6

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Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
35 40 45
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
50 55 60
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
65 70 75 80
Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
85 90 95
Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
100 105 110
Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
115 120 125
Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
130 135 140
Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
145 150 155 160
Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
165 170 175
His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
180 185 190
Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
195 200 205
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210 215 220
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